

IntelGenetics

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file us-10-033-742a-3.res made by tport on Fri 6 Feb 104 17:27:15-PST.

| | |
|--------------------------------|--------------------------|
| Query sequence being compared: | US-10-033-742A-3 (1-799) |
| Number of sequences searched: | 3 |
| Number of scores above cutoff: | 3 |

Number of scores above cutoff:

Number of scores above cutoff:

Results of the initial comparison of US-10-033-742A-3 (1-799) with:
File : 6096300.seq

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| Subject | Score | Stdev |
|---------|-------|-------|
| N | 458 | 10 |
| U | 51 | 0 |
| M | 51 | 0 |
| B | 102 | 0 |
| E | 153 | 0 |
| R | 204 | 0 |
| O | 254 | 0 |
| F | 305 | 10 |
| S | 305 | 10 |
| E | 356 | 0 |
| Q | 407 | 0 |
| U | 458 | 0 |
| E | 458 | 0 |
| N | 458 | 0 |
| C | 458 | 0 |
| S | 458 | 0 |

| | Unitary | K-tuple Joining penalty Window size | 4 30 5000 |
|---------------------|---------|---|-----------------|
| Similarity matrix | | | |
| Mismatch penalty | 1 | | |
| Gap penalty | 5.00 | | |
| Gap size penalty | 0.33 | | |
| Cutoff score | 1 | | |
| Randomization group | 0 | | |

| | | |
|---------|-------------|--------------------|
| Scores: | Mean | Standard Deviation |
| | 161 | 256.99 |
| | Median | |
| | 8 | |
| Times: | CPU | Total Elapsed |
| | 00:00:00.00 | 00:00:00.00 |

| | |
|--------------------------------|-----|
| Number of residues: | 873 |
| Number of sequences searched: | 3 |
| Number of scores above cutoff: | 3 |

Number of scores above cutoff:

Number of scores above cutoff:

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

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Applicants Copy

| Sequence Name | Description | Length | Score | Init. Opt. Score | Sig. Frame |
|---------------|-------------|--------|-------|------------------|------------|
| ----- | | | | | |

1. US-08-970-403-1 Sequence 1, Application US 821 458 757 1.16 0

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1. US-10-033-742A-3 (1-799)
US-08-970-403-1 Sequence 1, Application US/08970403

Initial Score = 458 Optimized Score = 757 Significance = 1.16
Residue Identity = 98% Matches = 778 Mismatches = 2
Gaps = 6 Conservative Substitutions = 0

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| | | | | | |
|------|---|---|----------------------------|---|---|
| Gaps | = | 6 | Conservative Substitutions | = | 0 |
|------|---|---|----------------------------|---|---|

| | | | | | |
|------|---|---|----------------------------|---|---|
| Gaps | = | 6 | Conservative Substitutions | = | 0 |
|------|---|---|----------------------------|---|---|

[illegible]

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720      730      740      750      760      770      780
TTCTTTGTTTATATGTTTGT-CTCCTAATTGTGTAATTGATTAATAAGAAAAACATTATTA
|||||
710      720      730      740      750      760      770
TTCTTTGTTTATATGTTTGTCTCTAATTGTGTAATTGATTAATAAGAAAAATTTAATA
|||||
790      X
GACAAATATT
|||||
GACAAATATTGAAATAAAGAAACAAAAGTTCTTCGTAAAAAAA
780      X      790      800      810      820

```